

SEQUENCE LISTING

<110> Gilbert, Michel
Wakarchuk, Warren W.
National Research Council of Canada

<120> Campylobacter Glycosyltransferases for Biosynthesis of
Gangliosides and Ganglioside Mimics

<130> 019633-000111US

<140> US 09/816,028

<141> 2001-03-21

<150> US 60/118,213

<151> 1999-02-01

<150> US 09/495,406

<151> 2000-01-31

<160> 49

<170> PatentIn Ver. 2.1

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<223> 11.5 kb PCR product from C. jejuni OH4384
including LOS biosynthesis locus

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Campylobacter sialyltransferase II (cstII) from C. jejuni
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biosynthesis locus)

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Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

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aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
                245                250                255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
                260                265                270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
                275                280                285

aaa gga aaa taa 876
Lys Gly Lys
                290

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<210> 3
<211> 291
<212> PRT
<213> Campylobacter jejuni

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<220>
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
      Campylobacter sialyltransferase II (cstII) from C. jejuni
      strain OH4384 (ORF 7a of lipooligosaccharide (LOS)
      biosynthesis locus)

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<400> 3
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1          5          10          15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
          20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
          35          40          45
Phe Tyr Asn Pro Ile Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65          70          75          80
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
          85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
          100          105          110
Lys Asp Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
          115          120          125
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130          135          140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145          150          155          160
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
          165          170          175
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
          180          185          190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
          195          200          205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210          215          220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225          230          235          240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
          245          250          255

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Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
260 265 270
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
275 280 285
Lys Gly Lys
290

<210> 4
<211> 876
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(876)
<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
Campylobacter sialyltransferase II (cstII) from C. jejuni
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
biosynthesis locus)

<400> 4
atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
1 5 10 15
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgc aat caa 96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
20 25 30
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa ttc aaa gca gta 144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val
35 40 45
ttt tac aat cct ggt ctt ttt ttt gaa caa tac tac act tta aaa cat 192
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
50 55 60
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
65 70 75 80
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
85 90 95
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
100 105 110
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ctc aat caa 384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln
115 120 125
aga att acc tca gga gtc tat atg tgt gca gta gct ata gcc cta gga 432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130 135 140

tac aaa gaa att tat ctt tct gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa ctg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 5

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> bifunctional alpha-2,3/alpha 2,8-sialyltransferase
Campylobacter sialyltransferase II (cstII) from C. jejuni
serotype O:10 (ORF 7a of lipooligosaccharide (LOS)
biosynthesis locus)

<400> 5

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Phe Lys Ala Val	
35 40 45	
Phe Tyr Asn Pro Gly Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	

Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Leu Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 6

<211> 876

<212> DNA

<213> *Campylobacter jejuni*

<220>

<221> CDS

<222> (1)..(876)

<223> *Campylobacter* alpha-2,3/alpha 2,8-sialyltransferase II
(cstII) from *C. jejuni* serotype O:41

<400> 6

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15

gat tat tca aga cta cca aat gat ttt gat gta ttt aga tgc aat caa 96
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30

ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gta 144
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35 40 45

ttt tac aat cct agt ctt ttt ttt gaa caa tac tac act tta aaa cat 192
 Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60

tta atc caa aat caa gaa tat gag acc gaa cta atc atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
ttt aac caa gct cat cta gaa aat caa aat ttt gta aaa act ttt tac	288
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttc aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttc aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgc aca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat gga tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa aaa aat ctt tta aaa ttg gct cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
aat ttt aaa aat gat aat tca cac tat atc gga cat agt aaa aat aca	576
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Glu Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac gaa ata aag cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu	
195 200 205	
tat tgt tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tat act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt aca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat att tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa taa	876
Lys Gly Lys	
290	

<210> 7
 <211> 291
 <212> PRT
 <213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (cstII) from C. jejuni serotype O:41

<400> 7

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Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1          5          10          15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
          20          25          30
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
          35          40          45
Phe Tyr Asn Pro Ser Leu Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
          50          55          60
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
          65          70          75          80
Phe Asn Gln Ala His Leu Glu Asn Gln Asn Phe Val Lys Thr Phe Tyr
          85          90          95
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
          100          105          110
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
          115          120          125
Arg Ile Thr Ser Gly Val Tyr Met Cys Thr Val Ala Ile Ala Leu Gly
          130          135          140
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
          145          150          155          160
Ser Tyr Ala Phe Asp Thr Lys Gln Lys Asn Leu Leu Lys Leu Ala Pro
          165          170          175
Asn Phe Lys Asn Asp Asn Ser His Tyr Ile Gly His Ser Lys Asn Thr
          180          185          190
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Glu Ile Lys Leu
          195          200          205
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
          210          215          220
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
          225          230          235          240
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Thr Lys
          245          250          255
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Ile Tyr Tyr Lys
          260          265          270
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
          275          280          285
Lys Gly Lys
          290

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<210> 8
 <211> 876
 <212> DNA
 <213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(876)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:19

<400> 8

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att	48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tcg cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	
tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255

 aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270

 ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285

 aaa gga aaa taa 876
 Lys Gly Lys
 290

<210> 9
 <211> 291
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni O:19

<400> 9
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val
 35 40 45
 Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270

Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 10
 <211> 294
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from C. jejuni strain NCTC 11168

<400> 10
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 1 5 10 15
 Lys Asn Ile Asp Tyr Lys Arg Leu Pro Lys Gln Phe Asp Val Phe Arg
 20 25 30
 Cys Asn Gln Phe Tyr Phe Glu Asp Arg Tyr Phe Val Gly Lys Asp Val
 35 40 45
 Lys Tyr Val Phe Phe Asn Pro Phe Val Phe Phe Glu Gln Tyr Tyr Thr
 50 55 60
 Ser Lys Lys Leu Ile Gln Asn Glu Glu Tyr Asn Ile Glu Asn Ile Val
 65 70 75 80
 Cys Ser Thr Ile Asn Leu Glu Tyr Ile Asp Gly Phe Gln Phe Val Asp
 85 90 95
 Asn Phe Glu Leu Tyr Phe Ser Asp Ala Phe Leu Gly His Glu Ile Ile
 100 105 110
 Lys Lys Leu Lys Asp Phe Phe Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr
 115 120 125
 Asn Arg Gln Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Thr Ala Val
 130 135 140
 Ala Leu Gly Tyr Lys Ser Ile Tyr Ile Ser Gly Ile Asp Phe Tyr Gln
 145 150 155 160
 Asp Thr Asn Asn Leu Tyr Ala Phe Asp Asn Asn Lys Lys Asn Leu Leu
 165 170 175
 Asn Lys Cys Thr Gly Phe Lys Asn Gln Lys Phe Lys Phe Ile Asn His
 180 185 190
 Ser Met Ala Cys Asp Leu Gln Ala Leu Asp Tyr Leu Met Lys Arg Tyr
 195 200 205
 Asp Val Asn Ile Tyr Ser Leu Asn Ser Asp Glu Tyr Phe Lys Leu Ala
 210 215 220
 Pro Asp Ile Gly Ser Asp Phe Val Leu Ser Lys Lys Pro Lys Lys Tyr
 225 230 235 240
 Ile Asn Asp Ile Leu Ile Pro Asp Lys Tyr Ala Gln Glu Arg Tyr Tyr
 245 250 255
 Gly Lys Lys Ser Arg Leu Lys Glu Asn Leu His Tyr Lys Leu Ile Lys
 260 265 270
 Asp Leu Ile Arg Leu Pro Ser Asp Ile Lys His Tyr Leu Lys Glu Lys
 275 280 285
 Tyr Ala Asn Lys Asn Arg
 290

<210> 11
 <211> 873
 <212> DNA
 <213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(873)

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:4

<400> 11

atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att	48
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa	96
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa gca gtg	144
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
ttt tac acc cct ggt ttc ttc ttt gag caa tac tac act tta aaa cat	192
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat	240
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac	288
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt	336
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa	384
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga	432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
tac aaa gaa att tat ctt tcg gga att gat ttt tat caa aat ggg tca	480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct	528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca	576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta	624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	

tat tgc tta tgt cct aac agt ctt tta gca aat ttt ata gaa cta gcg	672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala	
210 215 220	
cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act	720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr	
225 230 235 240	
aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa	768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys	
245 250 255	
aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag	816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys	
260 265 270	
ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc	864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe	
275 280 285	
aaa gga aaa	873
Lys Gly Lys	
290	

<210> 12

<211> 291

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:4

<400> 12

Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile	
1 5 10 15	
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln	
20 25 30	
Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Ala Val	
35 40 45	
Phe Tyr Thr Pro Gly Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His	
50 55 60	
Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn	
65 70 75 80	
Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr	
85 90 95	
Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu	
100 105 110	
Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln	
115 120 125	
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly	
130 135 140	
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser	
145 150 155 160	
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro	
165 170 175	
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr	
180 185 190	
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu	
195 200 205	

Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 13
 <211> 873
 <212> DNA
 <213> *Campylobacter jejuni*

<220>
 <221> CDS
 <222> (1)..(873)
 <223> *Campylobacter* alpha-2,3/alpha 2,8-sialyltransferase II
 (CstII) from *C. jejuni* O:36

<400> 13
 atg aaa aaa gtt att att gct gga aat gga cca agt tta aaa gaa att 48
 Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
 1 5 10 15
 gat tat tca agg cta cca aat gat ttt gat gta ttt aga tgt aat caa 96
 Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
 20 25 30
 ttt tat ttt gaa gat aaa tac tat ctt ggt aaa aaa tgc aaa aca gtg 144
 Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val
 35 40 45
 ttt tac acc cct aat ttc ttc ttt gag caa tac tac act tta aaa cat 192
 Phe Tyr Thr Pro Asn Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 tta atc caa aat caa gaa tat gag acc gaa cta att atg tgt tct aat 240
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 tac aac caa gct cat cta gaa aat gaa aat ttt gta aaa act ttt tac 288
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 gat tat ttt cct gat gct cat ttg gga tat gat ttt ttt aaa caa ctt 336
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 aaa gaa ttt aat gct tat ttt aaa ttt cac gaa att tat ttc aat caa 384
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125

aga att acc tca ggg gtc tat atg tgt gca gta gcc ata gcc cta gga 432
Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
130 135 140

tac aaa gaa att tat ctt tgc gga att gat ttt tat caa aat ggg tca 480
Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
145 150 155 160

tct tat gct ttt gat acc aaa caa gaa aat ctt tta aaa cta gcc cct 528
Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
165 170 175

gat ttt aaa aat gat cgc tca cac tat atc gga cat agt aaa aat aca 576
Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
180 185 190

gat ata aaa gct tta gaa ttt cta gaa aaa act tac aaa ata aaa cta 624
Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
195 200 205

tat tgc tta tgt cct aat agt ctt tta gca aat ttt ata gaa cta gcg 672
Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
210 215 220

cca aat tta aat tca aat ttt atc ata caa gaa aaa aat aac tac act 720
Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
225 230 235 240

aaa gat ata ctc ata cct tct agt gag gct tat gga aaa ttt tca aaa 768
Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
245 250 255

aat att aat ttt aaa aaa ata aaa att aaa gaa aat gtt tat tac aag 816
Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
260 265 270

ttg ata aaa gat cta tta aga tta cct agt gat ata aag cat tat ttc 864
Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
275 280 285

aaa gga aaa 873
Lys Gly Lys
290

<210> 14
<211> 291
<212> PRT
<213> Campylobacter jejuni

<220>
<223> Campylobacter alpha-2,3/alpha 2,8-sialyltransferase II
(CstII) from C. jejuni O:36

<400> 14
Met Lys Lys Val Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Glu Ile
1 5 10 15
Asp Tyr Ser Arg Leu Pro Asn Asp Phe Asp Val Phe Arg Cys Asn Gln
20 25 30

Phe Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Cys Lys Thr Val
 35 40 45
 Phe Tyr Thr Pro Asn Phe Phe Phe Glu Gln Tyr Tyr Thr Leu Lys His
 50 55 60
 Leu Ile Gln Asn Gln Glu Tyr Glu Thr Glu Leu Ile Met Cys Ser Asn
 65 70 75 80
 Tyr Asn Gln Ala His Leu Glu Asn Glu Asn Phe Val Lys Thr Phe Tyr
 85 90 95
 Asp Tyr Phe Pro Asp Ala His Leu Gly Tyr Asp Phe Phe Lys Gln Leu
 100 105 110
 Lys Glu Phe Asn Ala Tyr Phe Lys Phe His Glu Ile Tyr Phe Asn Gln
 115 120 125
 Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Ile Ala Leu Gly
 130 135 140
 Tyr Lys Glu Ile Tyr Leu Ser Gly Ile Asp Phe Tyr Gln Asn Gly Ser
 145 150 155 160
 Ser Tyr Ala Phe Asp Thr Lys Gln Glu Asn Leu Leu Lys Leu Ala Pro
 165 170 175
 Asp Phe Lys Asn Asp Arg Ser His Tyr Ile Gly His Ser Lys Asn Thr
 180 185 190
 Asp Ile Lys Ala Leu Glu Phe Leu Glu Lys Thr Tyr Lys Ile Lys Leu
 195 200 205
 Tyr Cys Leu Cys Pro Asn Ser Leu Leu Ala Asn Phe Ile Glu Leu Ala
 210 215 220
 Pro Asn Leu Asn Ser Asn Phe Ile Ile Gln Glu Lys Asn Asn Tyr Thr
 225 230 235 240
 Lys Asp Ile Leu Ile Pro Ser Ser Glu Ala Tyr Gly Lys Phe Ser Lys
 245 250 255
 Asn Ile Asn Phe Lys Lys Ile Lys Ile Lys Glu Asn Val Tyr Tyr Lys
 260 265 270
 Leu Ile Lys Asp Leu Leu Arg Leu Pro Ser Asp Ile Lys His Tyr Phe
 275 280 285
 Lys Gly Lys
 290

<210> 15
 <211> 1170
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <223> glycosyltransferase from C. jejuni strain OH4384
 (ORF 4a of lipooligosaccharide (LOS) biosynthesis
 locus)

<400> 15
 atgaagaaaa taggtgtagt tataccaatc tataatgtag aaaaatattt aagagaatgt 60
 ttagatagcg ttatcaatca aacttatact aacttagaaa tcatacttgt caatgatggg 120
 agcacagatg aacactcact caatattgca aaagaatata ccttaaaaga taaaagaata 180
 actctttttg ataagaaaaa tgggggttta agttcagcta gaaatatagg tatagaatac 240
 tttagcgggg aatataaatt aaaaaacaaa actcaacata taaaagaaaa ttctttaata 300
 gaatttcaat tggatggtta taatccttat aatatatata aagcatataa aagctctcaa 360
 gcttttaata atgaaaaaga tttaaccaat ttactttacc ctagtataga ttatattata 420
 ttcttagata gtgataatta ttggaaacta aactgcatag aagaatgcgt tataagaatg 480
 aaaaatgtgg atgtattgtg gtttgaccat gattgcacct atgaagacaa tataaaaaat 540
 aagcacaaaa aaacaaggat ggaaattttt gatttttaaaa aagaatgtat aatcactcca 600
 aaagaatatg caaatcgagc attaatgtga ggatctagag atatttcttt tggatggaat 660
 ggaatgattg attttaattt tttaaagcaa attaaactta aattttataaa ttttattatc 720
 aatgaagata tacacttttg gataattttg tttgctagtg ctaataaaat ttatgtttta 780
 tcacaaaagt tgtattttgtg tcgtttaaga gcaaacagta tatcaaatca tgataagaag 840

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attacaaaag caaatgtgtc agagtatttt aaagatatat atgaaacttt cggggaaaaac 900
gctaaggaag caaaaaatta tttaaaagca gcaagcaggg ttataactgc tttaaaattg 960
atagaatttt tttaaagatca aaaaaacgaa aatgcacttg ctataaaaaga aacattttta 1020
ccttgctatg ccaaaaaagc tttaatgatt aaaaaattta aaaaagatcc tttaaattta 1080
aaggaacaat tagttttaat taaacctttt attcaaacaa aacttcctta tgatatttgg 1140
aaattttggc aaaaaataaa aaatatatta 1170

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<210> 16

<211> 1044

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1044)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni strain OH4384 (ORF 5a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 16

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atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
  1          5          10          15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
          20          25          30

ata caa cga gat aaa atc gat tct tat tta cca aaa aaa act ctt gtg 144
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val
          35          40          45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct 192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
          50          55          60

att ata ggg gag ggg cat aaa gga tat ttt aat tat gat gaa aaa tct 240
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
          65          70          75          80

aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa 288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
          85          90          95

aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct 336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
          100          105          110

atc caa aga ggt gtt ata gga tat aat gat tgt acc gat gga agt gaa 384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
          115          120          125

gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata 432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
          130          135          140

aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat 480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
          145          150          155          160

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aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctt ata aaa ata gat gtg gat cat atc tat gat gct aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys	
180 185 190	
ctt tat aaa agc ttc tat ata cca aaa aac aaa tat gat gta gtt agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser	
195 200 205	
tat tca agg gtt gat att cac tat ttt aat gat aat ttt ttt ctt tgt	672
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys	
210 215 220	
aaa gat aat aat ggc aat ata ttg aaa gaa cca gga gat tgc ttg ctt	720
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu	
225 230 235 240	
atc aat aat tat aac tta aaa tgg aaa gaa gta tta att gac aga atc	768
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile	
245 250 255	
aat aac aat tgg aaa aaa gca aca aaa caa agt ttt tct tca aat ata	816
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile	
260 265 270	
cac tct tta gag caa tta aag tat aaa cac agg ata tta ttt cac act	864
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr	
275 280 285	
gaa tta aat aat tat cat ttt cct ttt tta aaa aaa cat aga gct caa	912
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln	
290 295 300	
gat att tat aaa tat aat tgg ata agt att gaa gaa ttt aaa aaa ttc	960
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe	
305 310 315 320	
tat tta caa aat att aat cat aaa ata gaa cct tct atg att tca aaa	1008
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys	
325 330 335	
gaa act cta aaa aaa ata ttc tta aca ttg ttt taa	1044
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe	
340 345	

<210> 17

<211> 347

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni strain OH4384 (ORF 5a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 17

Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
1 5 10 15
Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
20 25 30
Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Val
35 40 45
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
50 55 60
Ile Ile Gly Glu Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
65 70 75 80
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
85 90 95
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
100 105 110
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
115 120 125
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
130 135 140
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
145 150 155 160
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp
165 170 175
Glu Trp Leu Ile Lys Ile Asp Val Asp His Ile Tyr Asp Ala Lys Lys
180 185 190
Leu Tyr Lys Ser Phe Tyr Ile Pro Lys Asn Lys Tyr Asp Val Val Ser
195 200 205
Tyr Ser Arg Val Asp Ile His Tyr Phe Asn Asp Asn Phe Phe Leu Cys
210 215 220
Lys Asp Asn Asn Gly Asn Ile Leu Lys Glu Pro Gly Asp Cys Leu Leu
225 230 235 240
Ile Asn Asn Tyr Asn Leu Lys Trp Lys Glu Val Leu Ile Asp Arg Ile
245 250 255
Asn Asn Asn Trp Lys Lys Ala Thr Lys Gln Ser Phe Ser Ser Asn Ile
260 265 270
His Ser Leu Glu Gln Leu Lys Tyr Lys His Arg Ile Leu Phe His Thr
275 280 285
Glu Leu Asn Asn Tyr His Phe Pro Phe Leu Lys Lys His Arg Ala Gln
290 295 300
Asp Ile Tyr Lys Tyr Asn Trp Ile Ser Ile Glu Glu Phe Lys Lys Phe
305 310 315 320
Tyr Leu Gln Asn Ile Asn His Lys Ile Glu Pro Ser Met Ile Ser Lys
325 330 335
Glu Thr Leu Lys Lys Ile Phe Leu Thr Leu Phe
340 345

<210> 18

<211> 1608

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1608)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:1

<400> 18

atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att	48
Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile	
1 5 10 15	
gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa	96
Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys	
20 25 30	
aaa atc tac aat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac	144
Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn	
35 40 45	
tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	

att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	
aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt	912
Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg	
290 295 300	
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct	960
Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala	
305 310 315 320	
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta	1008
Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu	
325 330 335	
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca	1056
Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala	
340 345 350	
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat	1104
Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp	
355 360 365	
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga	1152
Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg	
370 375 380	
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg	1200
Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu	
385 390 395 400	
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa	1248
His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln	
405 410 415	
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta	1296
Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu	
420 425 430	
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt	1344
Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys	
435 440 445	
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa	1392
Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys	
450 455 460	
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca	1440
Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro	
465 470 475 480	

aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta 1488
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu
 485 490 495

ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata 1536
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile
 500 505 510

atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa 1584
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys
 515 520 525

aga gtt aat aat ata agc ttc tta 1608
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

<210> 19

<211> 536

<212> PRT

<213> Campylobacter jejuni

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:1

<400> 19

Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 Lys Ile Tyr Asn Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val
 50 55 60
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro
 65 70 75 80
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser
 85 90 95
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro
 100 105 110
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu
 115 120 125
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln
 130 135 140
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys
 145 150 155 160
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg
 165 170 175
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn
 180 185 190
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln
 195 200 205
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln
 210 215 220
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu
 260 265 270

Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg
 275 280 285
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg
 290 295 300
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala
 305 310 315 320
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu
 325 330 335
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala
 340 345 350
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp
 355 360 365
 Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg
 370 375 380
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu
 385 390 395 400
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln
 405 410 415
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu
 420 425 430
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys
 435 440 445
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys
 450 455 460
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro
 465 470 475 480
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu
 485 490 495
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile
 500 505 510
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys
 515 520 525
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

<210> 20

<211> 1056

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(1056)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:10

<400> 20

atg cta ttt caa tca tac ttt gtg aaa ata att tgc tta ttc atc cct 48
 Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
 1 5 10 15

ttt aga aaa att aga cat aaa ata aaa aaa aca ttt tta cta aaa aac 96
 Phe Arg Lys Ile Arg His Lys Ile Lys Lys Thr Phe Leu Leu Lys Asn
 20 25 30

ata caa cga gat aaa atc gat tct tat cta cca aaa aaa act ctt ata 144
 Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile
 35 40 45

caa att aat aaa tac aac aat gaa gat tta att aaa ctt aat aaa gct	192
Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala	
50 55 60	
att ata ggg ggg ggg cat aaa gga tat ttt aat tat gat gaa aaa tct	240
Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser	
65 70 75 80	
aaa gat cca aaa tct cct ttg aat cct tgg gct ttt ata cga gta aaa	288
Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys	
85 90 95	
aat gaa gct att acc tta aaa gct tct ctt gaa agc ata ttg cct gct	336
Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala	
100 105 110	
att caa aga ggt gtt ata gga tat aat gat tgc acc gat gga agt gaa	384
Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu	
115 120 125	
gaa ata att cta gaa ttt tgc aaa caa tat cct tca ttt ata cca ata	432
Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile	
130 135 140	
aaa tat cct tat gaa att caa att caa aac cca aaa tca gaa gaa aat	480
Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn	
145 150 155 160	
aaa ctc tat agc tat tat aat tat gtt gca agt ttt ata cca aaa gat	528
Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp	
165 170 175	
gag tgg ctc ata aaa ata gat gtg gat cat tat tat gat gca aaa aaa	576
Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys	
180 185 190	
tta tat aag agt ttt tat ata cct aga aaa aat tat cat gta att agt	624
Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser	
195 200 205	
tac tct agg ata gat ttt ata ttt aat gaa gaa aaa ttt tat gtt tat	672
Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr	
210 215 220	
cgg aat aag gag ggg gag att tta aaa gct cct gga gat tgt tta gca	720
Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala	
225 230 235 240	
ata caa aac act aac tta ttt tgg aaa gaa ata ctt att gaa gat gat	768
Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp	
245 250 255	
aca ttt aag tgg aat act gca aaa aat aat ata gag aat gca aaa tca	816
Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser	
260 265 270	
tat gaa att tta aaa gtt aga aat aga att tat ttt act aca gaa ctt	864
Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu	
275 280 285	

aat aat tat cat ttt cca ttt ata aaa aat tat aga aaa aat gat tat 912
 Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr
 290 295 300
 aag cag tta aat tgg gtt agc tta gat gat ttt att aaa aat tat aaa 960
 Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys
 305 310 315 320
 gaa aaa tta aaa aat caa ata gat ttt aaa atg cta gaa tac aaa aca 1008
 Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr
 325 330 335
 tta aaa aaa gtg tac aaa aag ctt aca tct tca gca agc gat aaa att 1056
 Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile
 340 345 350

<210> 21
 <211> 352
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni O:10

<400> 21
 Met Leu Phe Gln Ser Tyr Phe Val Lys Ile Ile Cys Leu Phe Ile Pro
 1 5 10 15
 Phe Arg Lys Ile Arg His Lys Ile Lys Thr Phe Leu Leu Lys Asn
 20 25 30
 Ile Gln Arg Asp Lys Ile Asp Ser Tyr Leu Pro Lys Lys Thr Leu Ile
 35 40 45
 Gln Ile Asn Lys Tyr Asn Asn Glu Asp Leu Ile Lys Leu Asn Lys Ala
 50 55 60
 Ile Ile Gly Gly Gly His Lys Gly Tyr Phe Asn Tyr Asp Glu Lys Ser
 65 70 75 80
 Lys Asp Pro Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val Lys
 85 90 95
 Asn Glu Ala Ile Thr Leu Lys Ala Ser Leu Glu Ser Ile Leu Pro Ala
 100 105 110
 Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser Glu
 115 120 125
 Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro Ile
 130 135 140
 Lys Tyr Pro Tyr Glu Ile Gln Ile Gln Asn Pro Lys Ser Glu Glu Asn
 145 150 155 160
 Lys Leu Tyr Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Lys Asp
 165 170 175
 Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys
 180 185 190
 Leu Tyr Lys Ser Phe Tyr Ile Pro Arg Lys Asn Tyr His Val Ile Ser
 195 200 205
 Tyr Ser Arg Ile Asp Phe Ile Phe Asn Glu Glu Lys Phe Tyr Val Tyr
 210 215 220
 Arg Asn Lys Glu Gly Glu Ile Leu Lys Ala Pro Gly Asp Cys Leu Ala
 225 230 235 240
 Ile Gln Asn Thr Asn Leu Phe Trp Lys Glu Ile Leu Ile Glu Asp Asp
 245 250 255
 Thr Phe Lys Trp Asn Thr Ala Lys Asn Asn Ile Glu Asn Ala Lys Ser
 260 265 270

Tyr Glu Ile Leu Lys Val Arg Asn Arg Ile Tyr Phe Thr Thr Glu Leu
 275 280 285
 Asn Asn Tyr His Phe Pro Phe Ile Lys Asn Tyr Arg Lys Asn Asp Tyr
 290 295 300
 Lys Gln Leu Asn Trp Val Ser Leu Asp Asp Phe Ile Lys Asn Tyr Lys
 305 310 315 320
 Glu Lys Leu Lys Asn Gln Ile Asp Phe Lys Met Leu Glu Tyr Lys Thr
 325 330 335
 Leu Lys Lys Val Tyr Lys Lys Leu Thr Ser Ser Ala Ser Asp Lys Ile
 340 345 350

<210> 22

<211> 945

<212> DNA

<213> Campylobacter jejuni

<220>

<221> CDS

<222> (1)..(945)

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:36

<400> 22

atg ctt aaa aaa atc att tct tta tat aaa aga tac tcg att tct aaa 48
 Met Leu Lys Lys Ile Ile Ser Leu Tyr Lys Arg Tyr Ser Ile Ser Lys
 1 5 10 15

aaa ttg gtt tta gat aat gag cat ttc att aag gaa aat aaa aac atc 96
 Lys Leu Val Leu Asp Asn Glu His Phe Ile Lys Glu Asn Lys Asn Ile
 20 25 30

tat gga aaa aaa cat aag ggc ttt ttt gac ttt gat gaa aag gct aag 144
 Tyr Gly Lys Lys His Lys Gly Phe Phe Asp Phe Asp Glu Lys Ala Lys
 35 40 45

gat gtg aaa tca ccc ctt aat cct tgg gga ttt atc agg gtt aaa aat 192
 Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn
 50 55 60

gaa gct tta acc cta aga gtt tct tta gaa agt ata cta cct gct tta 240
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu
 65 70 75 80

caa aga gga att ata gct tac aac gac tgt gat gat ggg agt gaa gag 288
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu
 85 90 95

ctt att tta gaa ttt tgc aag caa tat ccc aac ttc att gct aaa aaa 336
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys
 100 105 110

tat cct tat aaa gta gat cta gaa aat cct aaa aat gaa gaa aat aaa 384
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys
 115 120 125

ctt tac tct tat tac aat tgg gca gca tct ttt ata ccc tta gat gag 432
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu
 130 135 140

tgg ttt ata aaa atc gat gtg gat cat tac tac gat gcc aag aag ctt	480
Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu	
145 150 155 160	
tat aag agt ttt tat agg att gat caa gaa aat aaa gcc tta tgc tac	528
Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr	
165 170 175	
cca aga att aat ttt ata atc tta aat gga aat att tat gtg caa aat	576
Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn	
180 185 190	
agt gga aat tat gga ttc ata ggg ggg ggg gat caa ctc ttg att aaa	624
Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys	
195 200 205	
aga aga aat agt agc ttt ata gaa aga agg gtt tca aaa aaa agc caa	672
Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln	
210 215 220	
tgg ata gat cct aag gga ctt ata gaa gaa ctc tac tcc gag caa caa	720
Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
gtc tta tct caa gga gtg aaa ata cta caa gct ccc cta ctt cag tgg	768
Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp	
245 250 255	
cat ttt cct gcc tta aaa tac cgc cga aac gat tac caa caa tat tta	816
His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu	
260 265 270	
gat atc ttg agt tta gaa gaa ttt cag gcc ttt cat cgt aag agc aaa	864
Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys	
275 280 285	
gag gct aaa aaa ata gac ttt gcc atg cta aaa cgc cct gta atc gag	912
Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu	
290 295 300	
caa ata tta aag aaa ttt caa gga gag ata aaa	945
Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys	
305 310 315	

<210> 23

<211> 315

<212> PRT

<213> Campylobacter jejuni

<220>

<223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
transferase from C. jejuni O:36

<400> 23

Met	Leu	Lys	Lys	Ile	Ile	Ser	Leu	Tyr	Lys	Arg	Tyr	Ser	Ile	Ser	Lys
1				5					10				15		

Lys	Leu	Val	Leu	Asp	Asn	Glu	His	Phe	Ile	Lys	Glu	Asn	Lys	Asn	Ile
			20					25					30		

Tyr	Gly	Lys	Lys	His	Lys	Gly	Phe	Phe	Asp	Phe	Asp	Glu	Lys	Ala	Lys
		35				40						45			

Asp Val Lys Ser Pro Leu Asn Pro Trp Gly Phe Ile Arg Val Lys Asn
 50 55 60
 Glu Ala Leu Thr Leu Arg Val Ser Leu Glu Ser Ile Leu Pro Ala Leu
 65 70 75 80
 Gln Arg Gly Ile Ile Ala Tyr Asn Asp Cys Asp Asp Gly Ser Glu Glu
 85 90 95
 Leu Ile Leu Glu Phe Cys Lys Gln Tyr Pro Asn Phe Ile Ala Lys Lys
 100 105 110
 Tyr Pro Tyr Lys Val Asp Leu Glu Asn Pro Lys Asn Glu Glu Asn Lys
 115 120 125
 Leu Tyr Ser Tyr Tyr Asn Trp Ala Ala Ser Phe Ile Pro Leu Asp Glu
 130 135 140
 Trp Phe Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys Lys Leu
 145 150 155 160
 Tyr Lys Ser Phe Tyr Arg Ile Asp Gln Glu Asn Lys Ala Leu Cys Tyr
 165 170 175
 Pro Arg Ile Asn Phe Ile Ile Leu Asn Gly Asn Ile Tyr Val Gln Asn
 180 185 190
 Ser Gly Asn Tyr Gly Phe Ile Gly Gly Gly Asp Gln Leu Leu Ile Lys
 195 200 205
 Arg Arg Asn Ser Ser Phe Ile Glu Arg Arg Val Ser Lys Lys Ser Gln
 210 215 220
 Trp Ile Asp Pro Lys Gly Leu Ile Glu Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Val Leu Ser Gln Gly Val Lys Ile Leu Gln Ala Pro Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr Arg Arg Asn Asp Tyr Gln Gln Tyr Leu
 260 265 270
 Asp Ile Leu Ser Leu Glu Glu Phe Gln Ala Phe His Arg Lys Ser Lys
 275 280 285
 Glu Ala Lys Lys Ile Asp Phe Ala Met Leu Lys Arg Pro Val Ile Glu
 290 295 300
 Gln Ile Leu Lys Lys Phe Gln Gly Glu Ile Lys
 305 310 315

<210> 24
 <211> 1608
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(1608)
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni NCTC 11168

<400> 24
 atg act ttg ttt tat aaa att ata gct ttt tta aga ttg ctt aaa att 48
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 gat aaa aaa tta aaa ttt gat aat gaa tat ttt tta aac tta aat aaa 96
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 aaa atc tac gat gaa aag cat aaa ggt ttt ttt gat ttt gat cca aac 144
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45

tca aaa gat aca aaa tct cct tta aat cca tgg gct ttt ata aga gta	192
Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val	
50 55 60	
aaa aat gaa gcc act act tta aga gta tca ctt gaa agt atg tta cct	240
Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro	
65 70 75 80	
gcc ata caa aga ggt gtt ata gga tat aat gat tgt act gat gga agt	288
Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser	
85 90 95	
gaa gaa att att ttg gaa ttt tgc aaa caa tac cct tcg ttt ata cca	336
Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro	
100 105 110	
gta aaa tat ccc cat gag gtg caa att gaa aat ccg caa agc gaa gaa	384
Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu	
115 120 125	
aat aaa ctt cat agt tat tat aac tat gta gct agt ttt ata ccg caa	432
Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln	
130 135 140	
gat gag tgg ctt ata aaa ata gat gtg gat cat tac tat gat gca aaa	480
Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys	
145 150 155 160	
aaa tta tat aag agt ttt tat atg gca tca aaa aat act gct gtt aga	528
Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg	
165 170 175	
ttt cca aga att aat ttt tta ata cta gat aaa att gta att caa aat	576
Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn	
180 185 190	
ata gga gaa tgt ggt ttt atc gat gga ggg gat caa ttg tta att caa	624
Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln	
195 200 205	
aag tgc aat agt gta ttt ata gaa aga atg gtt tca aag caa agt cag	672
Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln	
210 215 220	
tgg att gat cct gaa aaa act gtg aaa gaa ttg tat tct gaa cag caa	720
Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln	
225 230 235 240	
att ata ccc aaa cat ata aaa atc tta caa gca gaa tta ctt caa tgg	768
Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp	
245 250 255	
cat ttt cct gct tta aaa tat cat aga aat gat tat caa aaa cat ttg	816
His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu	
260 265 270	
gat gct tta act tta gaa gat ttt aaa aaa atc cat tat aga cat aga	864
Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg	
275 280 285	

aaa ata aag aaa ata aat tat aca atg ctt gat gaa aaa gta att cgt Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg 290 295 300	912
gaa ata tta gat aaa ttt aaa ttg agt ggt aaa aaa atg act tta gct Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala 305 310 315 320	960
ata ata cct gct cga gct ggt tca aaa ggt ata aaa aat aaa aat tta Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu 325 330 335	1008
gct ctt ttg cat gat agg cct ttg ttg tat tat act atc aat gca gca Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala 340 345 350	1056
aaa aat tca aag tat gta gat aaa att gtt tta agt agt gat ggc gat Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp 355 360 365	1104
gat ata tta gaa tat gga caa act caa ggt gta gat gtg tta aaa aga Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg 370 375 380	1152
cct aaa gaa tta gcg cta gat gat aca act agt gat aag gtt gta ttg Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu 385 390 395 400	1200
cat acc ttg agt ttt tat aaa gat tat gaa aat att gtt tta tta caa His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln 405 410 415	1248
ccc act tct cct tta agg aca aat gta cat ata gat gaa gct ttt tta Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu 420 425 430	1296
aaa ttt aaa aat gaa aac tca aat gca tta ata agt gtt gta gaa tgt Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys 435 440 445	1344
gat aat aaa att tta aaa gct ttt ata gat gat aat ggt aac tta aaa Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys 450 455 460	1392
gga att tgt gat aac aaa tat cca ttt atg cct aga caa aaa tta cca Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro 465 470 475 480	1440
aaa act tat atg agt aat ggt gca att tat ata gta aag tca aat tta Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu 485 490 495	1488
ttt tta aat aac cca act ttt cta caa gaa aaa aca agt tgc tat ata Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile 500 505 510	1536
atg gac gaa aaa gct agt ttg gat ata gat aca aca gag gat tta aaa Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys 515 520 525	1584

aga gtt aat aat ata agc ttc tta
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

1608

<210> 25
 <211> 536
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,4 N-acetylgalactosaminyl (GalNAc)
 transferase from C. jejuni NCTC 11168

<400> 25
 Met Thr Leu Phe Tyr Lys Ile Ile Ala Phe Leu Arg Leu Leu Lys Ile
 1 5 10 15
 Asp Lys Lys Leu Lys Phe Asp Asn Glu Tyr Phe Leu Asn Leu Asn Lys
 20 25 30
 Lys Ile Tyr Asp Glu Lys His Lys Gly Phe Phe Asp Phe Asp Pro Asn
 35 40 45
 Ser Lys Asp Thr Lys Ser Pro Leu Asn Pro Trp Ala Phe Ile Arg Val
 50 55 60
 Lys Asn Glu Ala Thr Thr Leu Arg Val Ser Leu Glu Ser Met Leu Pro
 65 70 75 80
 Ala Ile Gln Arg Gly Val Ile Gly Tyr Asn Asp Cys Thr Asp Gly Ser
 85 90 95
 Glu Glu Ile Ile Leu Glu Phe Cys Lys Gln Tyr Pro Ser Phe Ile Pro
 100 105 110
 Val Lys Tyr Pro His Glu Val Gln Ile Glu Asn Pro Gln Ser Glu Glu
 115 120 125
 Asn Lys Leu His Ser Tyr Tyr Asn Tyr Val Ala Ser Phe Ile Pro Gln
 130 135 140
 Asp Glu Trp Leu Ile Lys Ile Asp Val Asp His Tyr Tyr Asp Ala Lys
 145 150 155 160
 Lys Leu Tyr Lys Ser Phe Tyr Met Ala Ser Lys Asn Thr Ala Val Arg
 165 170 175
 Phe Pro Arg Ile Asn Phe Leu Ile Leu Asp Lys Ile Val Ile Gln Asn
 180 185 190
 Ile Gly Glu Cys Gly Phe Ile Asp Gly Gly Asp Gln Leu Leu Ile Gln
 195 200 205
 Lys Cys Asn Ser Val Phe Ile Glu Arg Met Val Ser Lys Gln Ser Gln
 210 215 220
 Trp Ile Asp Pro Glu Lys Thr Val Lys Glu Leu Tyr Ser Glu Gln Gln
 225 230 235 240
 Ile Ile Pro Lys His Ile Lys Ile Leu Gln Ala Glu Leu Leu Gln Trp
 245 250 255
 His Phe Pro Ala Leu Lys Tyr His Arg Asn Asp Tyr Gln Lys His Leu
 260 265 270
 Asp Ala Leu Thr Leu Glu Asp Phe Lys Lys Ile His Tyr Arg His Arg
 275 280 285
 Lys Ile Lys Lys Ile Asn Tyr Thr Met Leu Asp Glu Lys Val Ile Arg
 290 295 300
 Glu Ile Leu Asp Lys Phe Lys Leu Ser Gly Lys Lys Met Thr Leu Ala
 305 310 315 320
 Ile Ile Pro Ala Arg Ala Gly Ser Lys Gly Ile Lys Asn Lys Asn Leu
 325 330 335
 Ala Leu Leu His Asp Arg Pro Leu Leu Tyr Tyr Thr Ile Asn Ala Ala
 340 345 350
 Lys Asn Ser Lys Tyr Val Asp Lys Ile Val Leu Ser Ser Asp Gly Asp
 355 360 365

Asp Ile Leu Glu Tyr Gly Gln Thr Gln Gly Val Asp Val Leu Lys Arg
 370 375 380
 Pro Lys Glu Leu Ala Leu Asp Asp Thr Thr Ser Asp Lys Val Val Leu
 385 390 395 400
 His Thr Leu Ser Phe Tyr Lys Asp Tyr Glu Asn Ile Val Leu Leu Gln
 405 410 415
 Pro Thr Ser Pro Leu Arg Thr Asn Val His Ile Asp Glu Ala Phe Leu
 420 425 430
 Lys Phe Lys Asn Glu Asn Ser Asn Ala Leu Ile Ser Val Val Glu Cys
 435 440 445
 Asp Asn Lys Ile Leu Lys Ala Phe Ile Asp Asp Asn Gly Asn Leu Lys
 450 455 460
 Gly Ile Cys Asp Asn Lys Tyr Pro Phe Met Pro Arg Gln Lys Leu Pro
 465 470 475 480
 Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile Val Lys Ser Asn Leu
 485 490 495
 Phe Leu Asn Asn Pro Thr Phe Leu Gln Glu Lys Thr Ser Cys Tyr Ile
 500 505 510
 Met Asp Glu Lys Ala Ser Leu Asp Ile Asp Thr Thr Glu Asp Leu Lys
 515 520 525
 Arg Val Asn Asn Ile Ser Phe Leu
 530 535

<210> 26

<211> 906

<212> DNA

<213> *Campylobacter jejuni*

<220>

<221> CDS

<222> (1)..(906)

<223> beta-1,3-galactosyltransferase from *C. jejuni* strain
 OH4384 (ORF 6a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 26

atg ttt aaa att tca atc atc tta cca act tat aat gtg gaa caa tat 48
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1 5 10 15

ata gca agg gca ata gaa agc tgt atc aat cag act ttt aaa gat ata 96
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
 20 25 30

gaa ata att gta gtt gat gat tgt gga aat gat aat agt ata aat ata 144
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile
 35 40 45

gcc aaa gaa tac tct aaa aaa gac aaa aga ata aaa ata atc cac aat 192
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn
 50 55 60

gaa aaa aac tta ggt ctt tta aga gca aga tat gaa ggt gtg aaa gta 240
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
 65 70 75 80

gca aac tct cct tat ata atg ttt tta gat cct gat gat tat ttg gaa 288
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
 85 90 95

cta aat gct tgt gaa gag tgt ata aaa att tta gat gaa cag gat gaa	336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu	
100 105 110	
gtt gat tta gtg ttt ttc aat gct att gtt gaa agt aat gtt att tca	384
Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser	
115 120 125	
tat aaa aag ttt gac ttt aat tct ggt ttt tat agc aaa aaa gag ttt	432
Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe	
130 135 140	
gta aaa aaa att att gca aag aaa aat tta tat tgg act atg tgg ggg	480
Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly	
145 150 155 160	
aaa ctt ata aga aag aaa ttg tat tta gaa gct ttt gcg agt tta aga	528
Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg	
165 170 175	
ctc gag aaa gat gtt aaa atc aat atg gct gaa gat gta ttg tta tat	576
Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr	
180 185 190	
tat cca atg tta agt caa gct caa aaa ata gca tat atg aac tgt aat	624
Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn	
195 200 205	
tta tat cat tac gtg cct aat aat aat tca att tgt aat act aag aat	672
Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn	
210 215 220	
gaa gtg ctt gtt aaa aat aat att caa gag ttg cag ttg gtt tta aac	720
Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn	
225 230 235 240	
tat tta agg caa aat tat att tta aac aag tat tgt agc gtt ctc tat	768
Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr	
245 250 255	
gtg cta att aaa tat ttg cta tat att caa ata tat aaa ata aaa aga	816
Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg	
260 265 270	
aca aaa tta atg gtt aca tta tta gct aaa ata aat att tta act tta	864
Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu	
275 280 285	
aaa att tta ttt aaa tat aaa aaa ttt tta aaa caa tgt taa	906
Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys	
290 295 300	

<210> 27

<211> 301

<212> PRT

<213> Campylobacter jejuni

<220>
 <223> beta-1,3-galactosyltransferase from C. jejuni strain
 OH4384 (ORF 6a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 27
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1 5 10 15
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
 20 25 30
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Asn Ser Ile Asn Ile
 35 40 45
 Ala Lys Glu Tyr Ser Lys Lys Asp Lys Arg Ile Lys Ile Ile His Asn
 50 55 60
 Glu Lys Asn Leu Gly Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
 65 70 75 80
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
 85 90 95
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Glu Gln Asp Glu
 100 105 110
 Val Asp Leu Val Phe Phe Asn Ala Ile Val Glu Ser Asn Val Ile Ser
 115 120 125
 Tyr Lys Lys Phe Asp Phe Asn Ser Gly Phe Tyr Ser Lys Lys Glu Phe
 130 135 140
 Val Lys Lys Ile Ile Ala Lys Lys Asn Leu Tyr Trp Thr Met Trp Gly
 145 150 155 160
 Lys Leu Ile Arg Lys Lys Leu Tyr Leu Glu Ala Phe Ala Ser Leu Arg
 165 170 175
 Leu Glu Lys Asp Val Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr
 180 185 190
 Tyr Pro Met Leu Ser Gln Ala Gln Lys Ile Ala Tyr Met Asn Cys Asn
 195 200 205
 Leu Tyr His Tyr Val Pro Asn Asn Asn Ser Ile Cys Asn Thr Lys Asn
 210 215 220
 Glu Val Leu Val Lys Asn Asn Ile Gln Glu Leu Gln Leu Val Leu Asn
 225 230 235 240
 Tyr Leu Arg Gln Asn Tyr Ile Leu Asn Lys Tyr Cys Ser Val Leu Tyr
 245 250 255
 Val Leu Ile Lys Tyr Leu Leu Tyr Ile Gln Ile Tyr Lys Ile Lys Arg
 260 265 270
 Thr Lys Leu Met Val Thr Leu Leu Ala Lys Ile Asn Ile Leu Thr Leu
 275 280 285
 Lys Ile Leu Phe Lys Tyr Lys Lys Phe Leu Lys Gln Cys
 290 295 300

<210> 28
 <211> 912
 <212> DNA
 <213> Campylobacter jejuni

<220>
 <221> CDS
 <222> (1)..(912)
 <223> Campylobacter glycosyltransferase B (CgtB) beta-1,3
 galactosyltransferase from C. jejuni serotype O:2
 (strain NCTC 11168)

<400> 28
atg agt caa att tcc atc ata cta cca act tat aat gtg gaa aaa tat 48
Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr
1 5 10 15

att gct aga gca tta gaa agt tgc att aac caa act ttt aaa gat ata 96
Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
20 25 30

gaa atc att gta gta gat gat tgt ggt aat gat aaa agt ata gat ata 144
Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile
35 40 45

gct aaa gag tat gct agt aaa gat gat aga ata aaa atc ata cat aat 192
Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn
50 55 60

gaa gag aat tta aag ctt tta aga gca aga tat gaa ggt gct aaa gta 240
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val
65 70 75 80

gca act tca cct tat atc atg ttt tta gat tct gat gat tat tta gaa 288
Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu
85 90 95

ctt aat gct tgc gaa gaa tgt att aaa att ttg gat atg ggt ggg ggg 336
Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly
100 105 110

ggt aaa att gat ttg ttg tgt ttt gaa gct ttt att acc aat gca aaa 384
Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys
115 120 125

aaa tca ata aaa aaa tta aat ata aaa caa gga aaa tac aac aac aaa 432
Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys
130 135 140

gaa ttt aca atg caa ata ctt aaa act aaa aat cca ttt tgg aca atg 480
Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met
145 150 155 160

tgg gct aaa ata atc aaa aaa gat att tat tta aaa gcc ttc aac atg 528
Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met
165 170 175

tta aat ctc aaa aaa gaa atc aaa ata aat atg gca gaa gat gcc tta 576
Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu
180 185 190

tta tat tat cct ttg aca ata tta tct aat gaa ata ttt tac tta aca 624
Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr
195 200 205

caa cct ttg tat acc cag cat gta aat agc aat tct ata aca aat aat 672
Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn
210 215 220

att aat tct tta gaa gct aat att caa gaa cat aaa att gtt tta aat 720
Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn
225 230 235 240

gtt tta aaa tca att aaa aat aaa aaa aca cct cta tat ttt cta att 768
 Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile
 245 250 255
 ata tat tta tta aaa att caa tta ttg aaa tat gaa caa aat ttt aat 816
 Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn
 260 265 270
 aaa aga aat ata aat ctt att tat tat aaa ata aat att tta tat caa 864
 Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln
 275 280 285
 aaa tat caa ttc aaa tgg aaa aaa ttt tta tat aat tta att ccg taa 912
 Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro
 290 295 300

<210> 29

<211> 303

<212> PRT

<213> Campylobacter jejuni

<220>

<223> Campylobacter glycosyltransferase B (CgtB) beta-1,3
 galactosyltransferase from C. jejuni serotype O:2
 (strain NCTC 11168)

<400> 29

Met Ser Gln Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Lys Tyr
 1 5 10 15
 Ile Ala Arg Ala Leu Glu Ser Cys Ile Asn Gln Thr Phe Lys Asp Ile
 20 25 30
 Glu Ile Ile Val Val Asp Asp Cys Gly Asn Asp Lys Ser Ile Asp Ile
 35 40 45
 Ala Lys Glu Tyr Ala Ser Lys Asp Asp Arg Ile Lys Ile Ile His Asn
 50 55 60
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Ala Lys Val
 65 70 75 80
 Ala Thr Ser Pro Tyr Ile Met Phe Leu Asp Ser Asp Asp Tyr Leu Glu
 85 90 95
 Leu Asn Ala Cys Glu Glu Cys Ile Lys Ile Leu Asp Met Gly Gly Gly
 100 105 110
 Gly Lys Ile Asp Leu Leu Cys Phe Glu Ala Phe Ile Thr Asn Ala Lys
 115 120 125
 Lys Ser Ile Lys Lys Leu Asn Ile Lys Gln Gly Lys Tyr Asn Asn Lys
 130 135 140
 Glu Phe Thr Met Gln Ile Leu Lys Thr Lys Asn Pro Phe Trp Thr Met
 145 150 155 160
 Trp Ala Lys Ile Ile Lys Lys Asp Ile Tyr Leu Lys Ala Phe Asn Met
 165 170 175
 Leu Asn Leu Lys Lys Glu Ile Lys Ile Asn Met Ala Glu Asp Ala Leu
 180 185 190
 Leu Tyr Tyr Pro Leu Thr Ile Leu Ser Asn Glu Ile Phe Tyr Leu Thr
 195 200 205
 Gln Pro Leu Tyr Thr Gln His Val Asn Ser Asn Ser Ile Thr Asn Asn
 210 215 220
 Ile Asn Ser Leu Glu Ala Asn Ile Gln Glu His Lys Ile Val Leu Asn
 225 230 235 240
 Val Leu Lys Ser Ile Lys Asn Lys Lys Thr Pro Leu Tyr Phe Leu Ile
 245 250 255

Ile Tyr Leu Leu Lys Ile Gln Leu Leu Lys Tyr Glu Gln Asn Phe Asn
260 265 270
Lys Arg Asn Ile Asn Leu Ile Tyr Tyr Lys Ile Asn Ile Leu Tyr Gln
275 280 285
Lys Tyr Gln Phe Lys Trp Lys Lys Phe Leu Tyr Asn Leu Ile Pro
290 295 300

<210> 30
<211> 891
<212> DNA
<213> Campylobacter jejuni

<220>
<221> CDS
<222> (1)..(891)
<223> beta-1,3 galactosyl transferase from C. jejuni 0:10

<400> 30
atg ttt aaa att tca atc atc ttg cca act tat aat gtg gaa caa tat 48
Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
1 5 10 15
ata gca agg gca ata gaa agt tgt atc aat cag act ttt aaa aat ata 96
Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile
20 25 30
gaa ata att gta gtt gat gat tgt gga agt gac aaa agt ata gat ata 144
Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile
35 40 45
gtt aaa gaa tat gcc aaa aaa gat gat aga ata aaa atc ata cat aat 192
Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn
50 55 60
gaa gaa aat tta aaa ctt tta aga gct aga tat gaa ggt gta aaa gta 240
Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
65 70 75 80
gca aac tct cct tat ata atg ttt tta gat cct gat gat tat tta gaa 288
Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
85 90 95
ctt aat gct tgt gaa gaa tgt atg aaa att tta aaa aac aat gaa ata 336
Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile
100 105 110
gat tta tta ttt ttt aat gca ttt gta ttg gaa aat aac aat aaa ata 384
Asp Leu Leu Phe Phe Asn Ala Phe Val Leu Glu Asn Asn Asn Lys Ile
115 120 125
gaa aga aag ttg aat ttt caa gaa aaa tgt tat gta aaa aaa gat ttt 432
Glu Arg Lys Leu Asn Phe Gln Glu Lys Cys Tyr Val Lys Lys Asp Phe
130 135 140
tta aaa gaa cta tta aaa act aaa aat tta ttt tgg aca gtg tgg gca 480
Leu Lys Glu Leu Leu Lys Thr Lys Asn Leu Phe Trp Thr Val Trp Ala
145 150 155 160

aaa gtc ata aaa aaa gaa tta tat ctc aag gct gtt ggt tta ata tcg 528
 Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser
 165 170 175

 cta gaa aat gct aaa ata aat atg gct gaa gat gtt tta tta tat tac 576
 Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr
 180 185 190

 cct ttg ata aat att tca aat act ata ttt cac ttg agt aaa aat tta 624
 Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu
 195 200 205

 tac aat tat caa ata aat aat ttc tct ata acc aaa aca tta aca ttg 672
 Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu
 210 215 220

 caa aat ata aaa aca aat ata caa gaa caa gat aat gtt cta tat ctt 720
 Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu
 225 230 235 240

 cta aag aag atg caa tat aat tac aat ttt aac tta act ttg ctt aaa 768
 Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys
 245 250 255

 tta att gag tat ttt tta tta att gaa aaa tac tca tta tca agc aag 816
 Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys
 260 265 270

 cga aat gtt ctt tgt ttt aaa atc aat att ttt ttt aaa aaa atc caa 864
 Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln
 275 280 285

 ttt aaa ttt tat cgc ttg ctg aag atg 891
 Phe Lys Phe Tyr Arg Leu Leu Lys Met
 290 295

<210> 31
 <211> 297
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> beta-1,3 galactosyl transferase from C. jejuni O:10

<400> 31
 Met Phe Lys Ile Ser Ile Ile Leu Pro Thr Tyr Asn Val Glu Gln Tyr
 1 5 10 15
 Ile Ala Arg Ala Ile Glu Ser Cys Ile Asn Gln Thr Phe Lys Asn Ile
 20 25 30
 Glu Ile Ile Val Val Asp Asp Cys Gly Ser Asp Lys Ser Ile Asp Ile
 35 40 45
 Val Lys Glu Tyr Ala Lys Lys Asp Asp Arg Ile Lys Ile Ile His Asn
 50 55 60
 Glu Glu Asn Leu Lys Leu Leu Arg Ala Arg Tyr Glu Gly Val Lys Val
 65 70 75 80
 Ala Asn Ser Pro Tyr Ile Met Phe Leu Asp Pro Asp Asp Tyr Leu Glu
 85 90 95
 Leu Asn Ala Cys Glu Glu Cys Met Lys Ile Leu Lys Asn Asn Glu Ile
 100 105 110

Asp Leu Leu Phe Phe Asn Ala Phe Val Leu Glu Asn Asn Asn Lys Ile
 115 120 125
 Glu Arg Lys Leu Asn Phe Gln Glu Lys Cys Tyr Val Lys Lys Asp Phe
 130 135 140
 Leu Lys Glu Leu Leu Lys Thr Lys Asn Leu Phe Trp Thr Val Trp Ala
 145 150 155 160
 Lys Val Ile Lys Lys Glu Leu Tyr Leu Lys Ala Val Gly Leu Ile Ser
 165 170 175
 Leu Glu Asn Ala Lys Ile Asn Met Ala Glu Asp Val Leu Leu Tyr Tyr
 180 185 190
 Pro Leu Ile Asn Ile Ser Asn Thr Ile Phe His Leu Ser Lys Asn Leu
 195 200 205
 Tyr Asn Tyr Gln Ile Asn Asn Phe Ser Ile Thr Lys Thr Leu Thr Leu
 210 215 220
 Gln Asn Ile Lys Thr Asn Ile Gln Glu Gln Asp Asn Val Leu Tyr Leu
 225 230 235 240
 Leu Lys Lys Met Gln Tyr Asn Tyr Asn Phe Asn Leu Thr Leu Leu Lys
 245 250 255
 Leu Ile Glu Tyr Phe Leu Leu Ile Glu Lys Tyr Ser Leu Ser Ser Lys
 260 265 270
 Arg Asn Val Leu Cys Phe Lys Ile Asn Ile Phe Phe Lys Lys Ile Gln
 275 280 285
 Phe Lys Phe Tyr Arg Leu Leu Lys Met
 290 295

<210> 32

<211> 295

<212> PRT

<213> Campylobacter jejuni

<220>

<223> lipid A biosynthesis acyltransferase from C.
 jejuni OH4384

<400> 32

Met Lys Asn Ser Asp Arg Ile Tyr Leu Ser Leu Tyr Tyr Ile Leu Lys
 1 5 10 15
 Phe Phe Val Thr Phe Met Pro Asp Cys Ile Leu His Phe Leu Ala Leu
 20 25 30
 Ile Val Ala Arg Ile Ala Phe His Leu Asn Lys Lys His Arg Lys Ile
 35 40 45
 Ile Asn Thr Asn Leu Gln Ile Cys Phe Pro Gln Tyr Thr Gln Lys Glu
 50 55 60
 Arg Asp Lys Leu Ser Leu Lys Ile Tyr Glu Asn Phe Ala Gln Phe Gly
 65 70 75 80
 Ile Asp Cys Leu Gln Asn Gln Asn Thr Thr Lys Glu Lys Ile Leu Asn
 85 90 95
 Lys Val Asn Phe Ile Asn Glu Asn Phe Leu Ile Asp Ala Leu Ala Leu
 100 105 110
 Lys Arg Pro Ile Ile Phe Thr Thr Ala His Tyr Gly Asn Trp Glu Ile
 115 120 125
 Leu Ser Leu Ala Tyr Ala Ala Lys Tyr Gly Ala Ile Ser Ile Val Gly
 130 135 140
 Lys Lys Leu Lys Ser Glu Val Met Tyr Glu Ile Leu Ser Gln Ser Arg
 145 150 155 160
 Thr Gln Phe Asp Ile Glu Leu Ile Asp Lys Lys Gly Gly Ile Arg Gln
 165 170 175
 Met Leu Ser Ala Leu Lys Lys Glu Arg Ala Leu Gly Ile Leu Thr Asp
 180 185 190

Gln Asp Cys Val Glu Asn Glu Ser Val Arg Leu Lys Phe Phe Asn Lys
 195 200 205
 Glu Val Asn Tyr Gln Met Gly Ala Ser Leu Ile Ala Gln Arg Ser Asn
 210 215 220
 Ala Leu Ile Ile Pro Val Tyr Ala Tyr Lys Glu Gly Gly Lys Phe Cys
 225 230 235 240
 Ile Glu Phe Phe Lys Ala Lys Asp Ser Gln Asn Ala Ser Leu Glu Glu
 245 250 255
 Leu Thr Leu Tyr Gln Ala Gln Ser Cys Glu Glu Met Ile Lys Lys Arg
 260 265 270
 Pro Trp Glu Tyr Phe Phe Phe His Arg Arg Phe Ala Ser Tyr Asn Glu
 275 280 285
 Glu Ile Tyr Lys Gly Ala Lys
 290 295

<210> 33

<211> 418

<212> PRT

<213> Campylobacter jejuni

<220>

<223> glycosyltransferase from C. jejuni OH4384 (ORF 3a
 of lipooligosaccharide (LOS) biosynthesis locus)

<400> 33

Met Asn Leu Lys Gln Ile Ser Val Ile Ile Ile Val Lys Asn Ala Glu
 1 5 10 15
 Gln Thr Leu Leu Glu Cys Leu Asn Ser Leu Lys Asp Phe Asp Glu Ile
 20 25 30
 Ile Leu Leu Asn Asn Glu Ser Ser Asp Asn Thr Leu Lys Ile Ala Asn
 35 40 45
 Glu Phe Lys Lys Asp Phe Ala Asn Leu Tyr Ile Tyr His Asn Ala Phe
 50 55 60
 Ile Gly Phe Gly Ala Leu Lys Asn Leu Ala Leu Ser Tyr Ala Lys Asn
 65 70 75 80
 Asp Trp Ile Leu Ser Ile Asp Ala Asp Glu Val Leu Glu Asn Glu Cys
 85 90 95
 Ile Lys Glu Leu Lys Asn Leu Lys Leu Gln Glu Asp Asn Ile Ile Ala
 100 105 110
 Leu Ser Arg Lys Asn Leu Tyr Lys Gly Glu Trp Ile Lys Ala Cys Gly
 115 120 125
 Trp Trp Pro Asp Tyr Val Leu Arg Ile Phe Asn Lys Asn Phe Thr Arg
 130 135 140
 Phe Asn Asp Asn Leu Val His Glu Ser Leu Val Leu Pro Ser Asn Ala
 145 150 155 160
 Lys Lys Ile Tyr Leu Lys Asn Gly Leu Lys His Tyr Ser Tyr Lys Asp
 165 170 175
 Ile Ser His Leu Ile Asp Lys Met Gln Tyr Tyr Ser Ser Leu Trp Ala
 180 185 190
 Lys Gln Asn Ile His Lys Lys Ser Gly Val Leu Lys Ala Asn Leu Arg
 195 200 205
 Ala Phe Trp Thr Phe Phe Arg Asn Tyr Phe Leu Lys Asn Gly Phe Leu
 210 215 220
 Tyr Gly Tyr Lys Gly Phe Ile Ile Ser Val Cys Ser Ala Leu Gly Thr
 225 230 235 240
 Phe Phe Lys Tyr Met Lys Leu Tyr Glu Leu Gln Arg Gln Lys Pro Lys
 245 250 255
 Thr Cys Ala Leu Ile Ile Ile Thr Tyr Asn Gln Lys Glu Arg Leu Lys
 260 265 270

Leu Val Leu Asp Ser Val Lys Asn Leu Ala Phe Leu Pro Asn Glu Val
 275 280 285
 Leu Ile Ala Asp Asp Gly Ser Lys Glu Asp Thr Ala Arg Leu Ile Glu
 290 295 300
 Glu Tyr Gln Lys Asp Phe Pro Cys Pro Leu Lys His Ile Trp Gln Glu
 305 310 315 320
 Asp Glu Gly Phe Lys Leu Ser Lys Ser Arg Asn Lys Thr Ile Lys Asn
 325 330 335
 Ala Asp Ser Glu Tyr Ile Ile Val Ile Asp Gly Asp Met Ile Leu Glu
 340 345 350
 Lys Asp Phe Ile Lys Glu His Leu Glu Phe Ala Gln Arg Lys Leu Phe
 355 360 365
 Leu Gln Gly Ser Arg Val Ile Leu Asn Lys Lys Glu Ser Glu Glu Ile
 370 375 380
 Leu Asn Lys Asp Asp Tyr Arg Ile Ile Phe Asn Lys Lys Asp Phe Lys
 385 390 395 400
 Ser Ser Lys Asn Ser Phe Leu Ala Lys Ile Phe Tyr Ser Leu Ser Lys
 405 410 415
 Lys Arg

<210> 34
 <211> 389
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> glycosyltransferase of C. jejuni OH4384 (ORF 4a of
 lipooligosaccharide (LOS) biosynthesis locus)

<400> 34
 Met Lys Lys Ile Gly Val Val Ile Pro Ile Tyr Asn Val Glu Lys Tyr
 1 5 10 15
 Leu Arg Glu Cys Leu Asp Ser Val Ile Asn Gln Thr Tyr Thr Asn Leu
 20 25 30
 Glu Ile Ile Leu Val Asn Asp Gly Ser Thr Asp Glu His Ser Leu Asn
 35 40 45
 Ile Ala Lys Glu Tyr Thr Leu Lys Asp Lys Arg Ile Thr Leu Phe Asp
 50 55 60
 Lys Lys Asn Gly Gly Leu Ser Ser Ala Arg Asn Ile Gly Ile Glu Tyr
 65 70 75 80
 Phe Ser Gly Glu Tyr Lys Leu Lys Asn Lys Thr Gln His Ile Lys Glu
 85 90 95
 Asn Ser Leu Ile Glu Phe Gln Leu Asp Gly Asn Asn Pro Tyr Asn Ile
 100 105 110
 Tyr Lys Ala Tyr Lys Ser Ser Gln Ala Phe Asn Asn Glu Lys Asp Leu
 115 120 125
 Thr Asn Phe Thr Tyr Pro Ser Ile Asp Tyr Ile Ile Phe Leu Asp Ser
 130 135 140
 Asp Asn Tyr Trp Lys Leu Asn Cys Ile Glu Glu Cys Val Ile Arg Met
 145 150 155 160
 Lys Asn Val Asp Val Leu Trp Phe Asp His Asp Cys Thr Tyr Glu Asp
 165 170 175
 Asn Ile Lys Asn Lys His Lys Lys Thr Arg Met Glu Ile Phe Asp Phe
 180 185 190
 Lys Lys Glu Cys Ile Ile Thr Pro Lys Glu Tyr Ala Asn Arg Ala Leu
 195 200 205
 Ser Val Gly Ser Arg Asp Ile Ser Phe Gly Trp Asn Gly Met Ile Asp
 210 215 220
 Phe Asn Phe Leu Lys Gln Ile Lys Leu Lys Phe Ile Asn Phe Ile Ile
 225 230 235 240

Gly Ala Cys Val Leu Glu Arg His Phe Thr Asp Ser Met His Arg Ser
 225 230 235 240
 Gly Pro Asp Ile Val Cys Ser Met Asp Thr Gln Ala Leu Lys Glu Leu
 245 250 255
 Ile Ile Gln Ser Glu Gln Met Ala Ile Met Arg Gly Asn Asn Glu Ser
 260 265 270
 Lys Lys Ala Ala Lys Gln Glu Gln Val Thr Ile Asp Phe Ala Phe Ala
 275 280 285
 Ser Val Val Ser Ile Lys Asp Ile Lys Lys Gly Glu Val Leu Ser Met
 290 295 300
 Asp Asn Ile Trp Val Lys Arg Pro Gly Leu Gly Gly Ile Ser Ala Ala
 305 310 315 320
 Glu Phe Glu Asn Ile Leu Gly Lys Lys Ala Leu Arg Asp Ile Glu Asn
 325 330 335
 Asp Thr Gln Leu Ser Tyr Glu Asp Phe Ala
 340 345

<210> 36

<211> 352

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> enzyme involved in sialic acid biosynthesis from
 C. jejuni OH4384 (ORF 9a of lipooligosaccharide (LOS)
 biosynthesis locus)

<400> 36

Met Tyr Arg Val Gln Asn Ser Ser Glu Phe Glu Leu Tyr Ile Phe Ala
 1 5 10 15
 Thr Gly Met His Leu Ser Lys Asn Phe Gly Tyr Thr Val Lys Glu Leu
 20 25 30
 Tyr Lys Asn Gly Phe Lys Asn Ile Tyr Glu Phe Ile Asn Tyr Asp Lys
 35 40 45
 Tyr Phe Ser Thr Asp Lys Ala Leu Ala Thr Thr Ile Asp Gly Phe Ser
 50 55 60
 Arg Tyr Val Asn Glu Leu Lys Pro Asp Leu Ile Val Val His Gly Asp
 65 70 75 80
 Arg Ile Glu Pro Leu Ala Ala Ala Ile Val Gly Ala Leu Asn Asn Ile
 85 90 95
 Leu Val Ala His Ile Glu Gly Gly Glu Ile Ser Gly Thr Ile Asp Asp
 100 105 110
 Ser Leu Arg His Ala Ile Ser Lys Leu Ala His Ile His Leu Val Asn
 115 120 125
 Asp Glu Phe Ala Lys Arg Arg Leu Met Gln Leu Gly Glu Asp Glu Lys
 130 135 140
 Ser Ile Phe Ile Ile Gly Ser Pro Asp Leu Glu Leu Leu Asn Asp Asn
 145 150 155 160
 Lys Ile Ser Leu Asn Glu Ala Lys Lys Tyr Tyr Asp Ile Asn Tyr Glu
 165 170 175
 Asn Tyr Ala Leu Leu Met Phe His Pro Val Thr Thr Glu Ile Thr Ser
 180 185 190
 Ile Lys Asn Gln Ala Asp Asn Leu Val Lys Ala Leu Ile Gln Ser Asn
 195 200 205
 Lys Asn Tyr Ile Val Ile Tyr Pro Asn Asn Asp Leu Gly Phe Glu Leu
 210 215 220
 Ile Leu Gln Ser Tyr Glu Glu Leu Lys Asn Asn Pro Arg Phe Lys Leu
 225 230 235 240
 Phe Pro Ser Leu Arg Phe Glu Tyr Phe Ile Thr Leu Leu Lys Asn Ala
 245 250 255

Asp Phe Ile Ile Gly Asn Ser Ser Cys Ile Leu Lys Glu Ala Leu Tyr
 260 265 270
 Leu Lys Thr Ala Gly Ile Leu Val Gly Ser Arg Gln Asn Gly Arg Leu
 275 280 285
 Gly Asn Glu Asn Thr Leu Lys Val Asn Ala Asn Ser Asp Glu Ile Leu
 290 295 300
 Lys Ala Ile Asn Thr Ile His Lys Lys Gln Asp Leu Phe Ser Ala Lys
 305 310 315 320
 Leu Glu Ile Leu Asp Ser Ser Lys Leu Phe Phe Glu Tyr Leu Gln Ser
 325 330 335
 Gly Glu Phe Phe Lys Leu Asn Thr Gln Lys Val Phe Lys Asp Ile Lys
 340 345 350

<210> 37

<211> 221

<212> PRT

<213> Campylobacter jejuni

<220>

<223> CMP-sialic acid synthetase from C. jejuni OH4384
 (ORF 10a of lipooligosaccharide (LOS) biosynthesis
 locus)

<400> 37

Met Ser Leu Ala Ile Ile Pro Ala Arg Gly Gly Ser Lys Gly Ile Lys
 1 5 10 15
 Asn Lys Asn Leu Val Leu Leu Asn Asn Lys Pro Leu Ile Tyr Tyr Thr
 20 25 30
 Ile Lys Ala Ala Leu Asn Thr Lys Ser Ile Ser Lys Val Val Val Ser
 35 40 45
 Ser Asp Ser Asp Glu Ile Leu Asn Tyr Ala Lys Ser Gln Asn Val Asp
 50 55 60
 Ile Leu Lys Arg Pro Ile Ser Leu Ala Gln Asp Asn Thr Thr Ser Asp
 65 70 75 80
 Lys Val Leu Leu His Ala Leu Lys Phe Tyr Lys Asp Tyr Glu Asp Val
 85 90 95
 Val Phe Leu Gln Pro Thr Ser Pro Leu Arg Thr Asn Ile His Ile Asp
 100 105 110
 Glu Ala Phe Asn Leu Tyr Lys Asn Ser Asn Ala Asn Ala Leu Ile Ser
 115 120 125
 Val Ser Glu Cys Asp Asn Lys Ile Leu Lys Ala Phe Val Cys Asn Glu
 130 135 140
 Tyr Gly Asp Leu Ala Gly Ile Cys Asn Asp Glu Tyr Pro Phe Met Pro
 145 150 155 160
 Arg Gln Lys Leu Pro Lys Thr Tyr Met Ser Asn Gly Ala Ile Tyr Ile
 165 170 175
 Leu Lys Ile Lys Glu Phe Leu Asn Asn Pro Ser Phe Leu Gln Ser Lys
 180 185 190
 Thr Lys His Phe Leu Met Asp Glu Ser Ser Ser Leu Asp Ile Asp Cys
 195 200 205
 Leu Glu Asp Leu Lys Lys Ala Glu Gln Ile Trp Lys Lys
 210 215 220

<210> 38

<211> 277

<212> PRT

<213> Campylobacter jejuni

<220>

<223> acetyltransferase from *C. jejuni* OH4384 (ORF 11a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 38

```
Met Glu Lys Ile Thr Leu Lys Cys Asn Lys Asn Ile Leu Asn Leu Leu
 1          5          10          15
Lys Gln Tyr Asn Ile Tyr Thr Lys Thr Tyr Ile Glu Asn Pro Arg Arg
          20          25          30
Phe Ser Arg Leu Lys Thr Lys Asp Phe Ile Thr Phe Pro Leu Glu Asn
          35          40          45
Asn Gln Leu Glu Ser Val Ala Gly Leu Gly Ile Glu Glu Tyr Cys Ala
          50          55          60
Phe Lys Phe Ser Asn Ile Leu His Glu Met Asp Ser Phe Ser Phe Ser
65          70          75          80
Gly Ser Phe Leu Pro His Tyr Thr Lys Val Gly Arg Tyr Cys Ser Ile
          85          90          95
Ser Asp Gly Val Ser Met Phe Asn Phe Gln His Pro Met Asp Arg Ile
          100          105          110
Ser Thr Ala Ser Phe Thr Tyr Glu Thr Asn His Ser Phe Ile Asn Asp
          115          120          125
Ala Cys Gln Asn His Ile Asn Lys Thr Phe Pro Ile Val Asn His Asn
          130          135          140
Pro Ser Ser Ser Ile Thr His Leu Ile Ile Gln Asp Asp Val Trp Ile
145          150          155          160
Gly Lys Asp Val Leu Leu Lys Gln Gly Ile Thr Leu Gly Thr Gly Cys
          165          170          175
Val Ile Gly Gln Arg Ala Val Val Thr Lys Asp Val Pro Pro Tyr Ala
          180          185          190
Ile Val Ala Gly Ile Pro Ala Lys Ile Ile Lys Tyr Arg Phe Asp Glu
          195          200          205
Lys Thr Ile Glu Arg Leu Leu Lys Ile Gln Trp Trp Lys Tyr His Phe
210          215          220
Ala Asp Phe Tyr Asp Ile Asp Leu Asn Leu Lys Ile Asn Gln Tyr Leu
225          230          235          240
Asp Leu Leu Glu Glu Lys Ile Ile Lys Lys Ser Ile Ser Tyr Tyr Asn
          245          250          255
Pro Asn Lys Leu Tyr Phe Arg Asp Ile Leu Glu Leu Lys Ser Lys Lys
          260          265          270
Ile Phe Asn Leu Phe
          275
```

<210> 39

<211> 270

<212> PRT

<213> *Campylobacter jejuni*

<220>

<223> glycosyltransferase from *C. jejuni* OH4384 (ORF 12a
of lipooligosaccharide (LOS) biosynthesis locus)

<400> 39

```
Met Pro Gln Leu Ser Ile Ile Ile Pro Leu Phe Asn Ser Cys Asp Phe
 1          5          10          15
Ile Ser Arg Ala Leu Gln Ser Cys Ile Asn Gln Thr Leu Lys Asp Ile
          20          25          30
Glu Ile Leu Ile Ile Asp Asp Lys Ser Lys Asp Asn Ser Leu Asn Met
          35          40          45
Val Leu Glu Phe Ala Lys Lys Asp Pro Arg Ile Lys Ile Phe Gln Asn
          50          55          60
```


Glu	Glu	Asn	Leu	Gly	Thr	Phe	Ala	Ser	Arg	Asn	Leu	Gly	Val	Leu	His
65					70					75					80
Ser	Ser	Ser	Asp	Phe	Ile	Met	Phe	Leu	Asp	Ser	Asp	Asp	Phe	Leu	Thr
				85					90					95	
Pro	Asp	Ala	Cys	Glu	Ile	Ala	Phe	Lys	Glu	Met	Lys	Lys	Gly	Phe	Asp
			100					105					110		
Leu	Leu	Cys	Phe	Asp	Ala	Phe	Val	His	Arg	Val	Lys	Thr	Lys	Gln	Phe
		115					120					125			
Tyr	Arg	Phe	Lys	Gln	Asp	Glu	Val	Phe	Asn	Gln	Lys	Glu	Phe	Leu	Glu
	130					135					140				
Phe	Leu	Ser	Lys	Gln	Arg	His	Phe	Cys	Trp	Ser	Val	Trp	Ala	Lys	Cys
145					150					155					160
Phe	Lys	Lys	Asp	Ile	Ile	Leu	Lys	Ser	Phe	Glu	Lys	Ile	Lys	Ile	Asp
			165						170					175	
Glu	Arg	Leu	Asn	Tyr	Gly	Glu	Asp	Val	Leu	Phe	Cys	Tyr	Ile	Tyr	Phe
			180					185					190		
Met	Phe	Cys	Glu	Lys	Ile	Ala	Val	Phe	Lys	Thr	Cys	Ile	Tyr	His	Tyr
		195					200					205			
Glu	Phe	Asn	Pro	Asn	Gly	Arg	Tyr	Glu	Asn	Lys	Asn	Lys	Glu	Ile	Leu
	210					215					220				
Asn	Gln	Asn	Tyr	His	Asp	Lys	Lys	Lys	Ser	Asn	Glu	Ile	Ile	Lys	Lys
225					230					235					240
Leu	Ser	Lys	Glu	Phe	Ala	His	Asp	Glu	Phe	His	Gln	Lys	Leu	Phe	Glu
				245					250					255	
Val	Leu	Lys	Arg	Glu	Glu	Ala	Gly	Val	Lys	Asn	Arg	Leu	Lys		
			260					265					270		

<210> 40
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ42 primer in
 heptosyltransferase-II used to amplify LPS core
 biosynthesis locus

<400> 40
 gccattaccg tatcgcttaa ccagg

25

<210> 41
 <211> 25
 <212> DNA
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:CJ43 primer in
 heptosyltransferase-I used to amplify LPS core
 biosynthesis locus

<400> 41
 aaagaatacg aatttgctaa agagg

25

<210> 42
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-106 3'
 primer used to amplify and clone ORF 5a

 <400> 42 41
 cctaggtcga cttaaaacaa tgtaagaat atttttttta g

 <210> 43
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CJ-157 5'
 primer used to amplify and clone ORF 5a

 <400> 43 37
 cttaggaggt catatgctat ttcaatcata ctttgtg

 <210> 44
 <211> 37
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CJ-105 3'
 primer used to amplify and clone ORF 6a

 <400> 44 37
 cctaggtcga cctctaaaaa aaatattctt aacattg

 <210> 45
 <211> 39
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CJ-133 5'
 primer used to amplify and clone ORF 6a

 <400> 45 39
 cttaggaggt catatgttta aaatttcaat catcttacc

 <210> 46
 <211> 41
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> Description of Artificial Sequence:CJ-131 5'
 primer used to amplify and clone ORF 7a

 <400> 46 41
 cttaggaggt catatgaaaa aagttattat tgctggaaat g

<210> 47
 <211> 41
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:CJ-132 3'
 primer used to amplify and clone ORF 7a

<400> 47
 cctagggtcga cttatttttcc ttgaaataa tgctttatat c

41

<210> 48
 <211> 322
 <212> PRT
 <213> Campylobacter jejuni

<220>
 <223> Campylobacter alpha-2,3-sialyltransferase I (Cst-I)
 from C. jejuni OH4384

<400> 48
 Met Thr Arg Thr Arg Met Glu Asn Glu Leu Ile Val Ser Lys Asn Met
 1 5 10 15
 Gln Asn Ile Ile Ala Gly Asn Gly Pro Ser Leu Lys Asn Ile Asn
 20 25 30
 Tyr Lys Arg Leu Pro Arg Glu Tyr Asp Val Phe Arg Cys Asn Gln Phe
 35 40 45
 Tyr Phe Glu Asp Lys Tyr Tyr Leu Gly Lys Lys Ile Lys Ala Val Phe
 50 55 60
 Phe Asn Pro Gly Val Phe Leu Gln Gln Tyr His Thr Ala Lys Gln Leu
 65 70 75 80
 Ile Leu Lys Asn Glu Tyr Glu Ile Lys Asn Ile Phe Cys Ser Thr Phe
 85 90 95
 Asn Leu Pro Phe Ile Glu Ser Asn Asp Phe Leu His Gln Phe Tyr Asn
 100 105 110
 Phe Phe Pro Asp Ala Lys Leu Gly Tyr Glu Val Ile Glu Asn Leu Lys
 115 120 125
 Glu Phe Tyr Ala Tyr Ile Lys Tyr Asn Glu Ile Tyr Phe Asn Lys Arg
 130 135 140
 Ile Thr Ser Gly Val Tyr Met Cys Ala Ile Ala Ile Ala Leu Gly Tyr
 145 150 155 160
 Lys Thr Ile Tyr Leu Cys Gly Ile Asp Phe Tyr Glu Gly Asp Val Ile
 165 170 175
 Tyr Pro Phe Glu Ala Met Ser Thr Asn Ile Lys Thr Ile Phe Pro Gly
 180 185 190
 Ile Lys Asp Phe Lys Pro Ser Asn Cys His Ser Lys Glu Tyr Asp Ile
 195 200 205
 Glu Ala Leu Lys Leu Leu Lys Ser Ile Tyr Lys Val Asn Ile Tyr Ala
 210 215 220
 Leu Cys Asp Asp Ser Ile Leu Ala Asn His Phe Pro Leu Ser Ile Asn
 225 230 235 240
 Ile Asn Asn Asn Phe Thr Leu Glu Asn Lys His Asn Asn Ser Ile Asn
 245 250 255
 Asp Ile Leu Leu Thr Asp Asn Thr Pro Gly Val Ser Phe Tyr Lys Asn
 260 265 270
 Gln Leu Lys Ala Asp Asn Lys Ile Met Leu Asn Phe Tyr Asn Ile Leu
 275 280 285
 His Ser Lys Asp Asn Leu Ile Lys Phe Leu Asn Lys Glu Ile Ala Val
 290 295 300

Leu Lys Lys Gln Thr Thr Gln Arg Ala Lys Ala Arg Ile Gln Asn His
 305 310 315 320
 Leu Ser

<210> 49
 <211> 231
 <212> PRT
 <213> Haemophilus influenzae

<220>
 <223> putative ORF from GenBank #U32720

<400> 49
 Met Gln Leu Ile Lys Asn Asn Glu Tyr Glu Tyr Ala Asp Ile Ile Leu
 1 5 10 15
 Ser Ser Phe Val Asn Leu Gly Asp Ser Glu Leu Lys Lys Ile Lys Asn
 20 25 30
 Val Gln Lys Leu Leu Thr Gln Val Asp Ile Gly His Tyr Tyr Leu Asn
 35 40 45
 Lys Leu Pro Ala Phe Asp Ala Tyr Leu Gln Tyr Asn Glu Leu Tyr Glu
 50 55 60
 Asn Lys Arg Ile Thr Ser Gly Val Tyr Met Cys Ala Val Ala Thr Val
 65 70 75 80
 Met Gly Tyr Lys Asp Leu Tyr Leu Thr Gly Ile Asp Phe Tyr Gln Glu
 85 90 95
 Lys Gly Asn Pro Tyr Ala Phe His His Gln Lys Glu Asn Ile Ile Lys
 100 105 110
 Leu Leu Pro Ser Phe Ser Gln Asn Lys Ser Gln Ser Asp Ile His Ser
 115 120 125
 Met Glu Tyr Asp Leu Asn Ala Leu Tyr Phe Leu Gln Lys His Tyr Gly
 130 135 140
 Val Asn Ile Tyr Cys Ile Ser Pro Glu Ser Pro Leu Cys Asn Tyr Phe
 145 150 155 160
 Pro Leu Ser Pro Leu Asn Asn Pro Ile Thr Phe Ile Leu Glu Glu Lys
 165 170 175
 Lys Asn Tyr Thr Gln Asp Ile Leu Ile Pro Pro Lys Phe Val Tyr Lys
 180 185 190
 Lys Ile Gly Ile Tyr Ser Lys Pro Arg Ile Tyr Gln Asn Leu Ile Phe
 195 200 205
 Arg Leu Ile Trp Asp Ile Leu Arg Leu Pro Asn Asp Ile Lys His Ala
 210 215 220
 Leu Lys Ser Arg Lys Trp Asp
 225 230